

WEST Search History

DATE: Wednesday, May 25, 2005

| <u>Hide?</u> | <u>Set Name</u> | <u>Query</u> | <u>Hit Count</u> |
|--------------------------|--|---|------------------|
| | <i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i> | | |
| <input type="checkbox"/> | L32 | l8 and l30 | 5 |
| <input type="checkbox"/> | L31 | L30 and l21 | 33 |
| <input type="checkbox"/> | L30 | (514/2)![CCLS] | 6636 |
| <input type="checkbox"/> | L29 | (514)![CCLS] | 0 |
| <input type="checkbox"/> | L28 | 20020119129.pn. | 1 |
| <input type="checkbox"/> | L27 | 6093565.pn. | 1 |
| <input type="checkbox"/> | L26 | 6242587.pn. | 1 |
| <input type="checkbox"/> | L25 | L24 and L17 | 6 |
| <input type="checkbox"/> | L24 | L23 or L9 | 154 |
| <input type="checkbox"/> | L23 | L4.ti. | 38 |
| <input type="checkbox"/> | L22 | L9 and L17 | 6 |
| <input type="checkbox"/> | L21 | L20 and L17 | 6570 |
| <input type="checkbox"/> | L20 | cnB or (CN with beta) or (cn with B) canB or (can with b) | 408983 |
| <input type="checkbox"/> | L19 | cnB or (CN with beta) or canB or (can with b) | 409019 |
| <input type="checkbox"/> | L18 | L17 and L4 | 242 |
| <input type="checkbox"/> | L17 | L12 or L13 or L14 or L15 or L16 | 62432 |
| <input type="checkbox"/> | L16 | chen.in. | 43635 |
| <input type="checkbox"/> | L15 | lian.in. | 690 |
| <input type="checkbox"/> | L14 | gao.in. | 2563 |
| <input type="checkbox"/> | L13 | yan.in. | 4377 |
| <input type="checkbox"/> | L12 | wei.in. | 14630 |
| <input type="checkbox"/> | L11 | L10 not @ay>1998 | 19 |
| <input type="checkbox"/> | L10 | L9 and L5 | 82 |
| <input type="checkbox"/> | L9 | L7 or L8 | 154 |
| <input type="checkbox"/> | L8 | L4.ab. | 79 |
| <input type="checkbox"/> | L7 | L4.clm. | 107 |
| <input type="checkbox"/> | L6 | L5 and L4 | 1121 |
| <input type="checkbox"/> | L5 | cancer\$ or tumor\$ or neoplas\$ | 163081 |
| <input type="checkbox"/> | L4 | calcineurin | 1464 |
| <input type="checkbox"/> | L3 | L2 or L1 | 2 |
| <input type="checkbox"/> | L2 | 6093565.pn. | 1 |

☐ L1 6242587.pn.

1

END OF SEARCH HISTORY

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 71 Seconds
(without alignments)
920.599 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCVVGGGLDIHKKMVVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|---------------|-------|-------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 870 | 100.0 | 169 | 7 | ADE55926 | Ade55926 Rat Prote |
| 2 | 870 | 100.0 | 169 | 7 | ADE55928 | Ade55928 Human Pro |
| 3 | 870 | 100.0 | 170 | 2 | AAW64200 | Aaw64200 Human cal |
| 4 | 870 | 100.0 | 170 | 3 | AAB09978 | Aab09978 Human HCN |
| 5 | 870 | 100.0 | 170 | 8 | ADI27357 | Adi27357 Human cal |
| 6 | 762 | 87.6 | 170 | 4 | ABB60493 | Abb60493 Drosophil |
| 7 | 739 | 84.9 | 162 | 4 | ABB65554 | Abb65554 Drosophil |
| 8 | 733 | 84.3 | 170 | 4 | AAO14411 | Aao14411 Calcineur |
| 9 | 733 | 84.3 | 173 | 4 | AAB64410 | Aab64410 Amino aci |

| | | | | | | | | |
|----|-------|------|-----|---|----------|----------|-----------|-----|
| 10 | 733 | 84.3 | 173 | 6 | ADA55632 | Ada55632 | Human | pro |
| 11 | 733 | 84.3 | 187 | 4 | AAU87327 | Aau87327 | Novel | cen |
| 12 | 733 | 84.3 | 187 | 8 | ADI54642 | Adi54642 | Novel | hum |
| 13 | 733 | 84.3 | 189 | 4 | AAM95239 | Aam95239 | Human | rep |
| 14 | 733 | 84.3 | 189 | 4 | AAM43639 | Aam43639 | Human | pol |
| 15 | 733 | 84.3 | 189 | 4 | AAM43564 | Aam43564 | Human | pol |
| 16 | 733 | 84.3 | 189 | 4 | AAU19951 | Aau19951 | Novel | hum |
| 17 | 733 | 84.3 | 189 | 4 | ABB95936 | Abb95936 | Human | tes |
| 18 | 733 | 84.3 | 189 | 4 | AAU87615 | Aau87615 | Novel | cen |
| 19 | 733 | 84.3 | 189 | 8 | ADI54930 | Adi54930 | Novel | hum |
| 20 | 733 | 84.3 | 189 | 8 | ADM24660 | Adm24660 | Human | PRO |
| 21 | 733 | 84.3 | 189 | 8 | ADM24585 | Adm24585 | Human | PRO |
| 22 | 728 | 83.7 | 170 | 3 | AAB09977 | Aab09977 | Human | CNB |
| 23 | 501 | 57.6 | 197 | 8 | ADS24073 | Ads24073 | Bacterial | |
| 24 | 496 | 57.0 | 175 | 2 | AAU00881 | Aay00881 | Calcineur | |
| 25 | 496 | 57.0 | 175 | 8 | ADS43790 | Ads43790 | Bacterial | |
| 26 | 429.5 | 49.4 | 195 | 8 | ADS44352 | Ads44352 | Bacterial | |
| 27 | 429 | 49.3 | 185 | 8 | ADN21422 | Adn21422 | Bacterial | |
| 28 | 393 | 45.2 | 90 | 3 | AAG02990 | Aag02990 | Human | sec |
| 29 | 373.5 | 42.9 | 178 | 3 | AAU77951 | Aay77951 | A. thalia | |
| 30 | 340.5 | 39.1 | 195 | 6 | ABG74662 | Abg74662 | Murine Ca | |
| 31 | 337.5 | 38.8 | 194 | 6 | ABG74856 | Abg74856 | Human cal | |
| 32 | 337.5 | 38.8 | 194 | 7 | ADD46021 | Add46021 | Human Pro | |
| 33 | 337.5 | 38.8 | 194 | 7 | ADE59921 | Ade59921 | Human Pro | |
| 34 | 337.5 | 38.8 | 194 | 7 | ADE61228 | Ade61228 | Human Pro | |
| 35 | 337.5 | 38.8 | 194 | 7 | ADE59917 | Ade59917 | Human Pro | |
| 36 | 337.5 | 38.8 | 195 | 6 | ABG74661 | Abg74661 | Human Ca2 | |
| 37 | 337.5 | 38.8 | 195 | 6 | ABU89717 | Abu89717 | Protein d | |
| 38 | 321.5 | 37.0 | 189 | 4 | ABB58936 | Abb58936 | Drosophil | |
| 39 | 316.5 | 36.4 | 213 | 8 | ADN23634 | Adn23634 | Bacterial | |
| 40 | 303.5 | 34.9 | 195 | 8 | ADN23801 | Adn23801 | Bacterial | |
| 41 | 292 | 33.6 | 207 | 4 | AAM43642 | Aam43642 | Human pol | |
| 42 | 292 | 33.6 | 207 | 4 | AAU19948 | Aau19948 | Novel hum | |
| 43 | 292 | 33.6 | 207 | 4 | AAU87620 | Aau87620 | Novel cen | |
| 44 | 292 | 33.6 | 207 | 8 | ADI54935 | Adi54935 | Novel hum | |
| 45 | 292 | 33.6 | 207 | 8 | ADM24663 | Adm24663 | Human PRO | |

RESULT 3

AAW64200

ID AAW64200 standard; protein; 170 AA.

XX

AC AAW64200;

XX

DT 09-NOV-1998 (first entry)

XX

DE Human calcineurin.

XX

KW Calcineurin; interferon receptor 1 binding protein; IR1B1; human.

XX

OS Homo sapiens.

XX

PN WO9831796-A1.

XX

PD 23-JUL-1998.

XX

PF 15-JAN-1998; 98WO-US000671.

XX
 PR 15-JAN-1997; 97US-0035636P.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (MCIN/) MCINNIS P A.
 XX
 PI Revel M, Abramovitch C, Chebath JE;
 XX
 DR WPI; 1998-414096/35.
 XX
 PT New isolated interferon receptor binding proteins - used to develop
 PT products for modulating sensitivity to interferon, e.g. in the treatment
 PT of tumours or for prolonging graft survival.
 XX
 PS Example 2; Page 35-36; 64pp; English.
 XX
 CC This polypeptide comprises the human calcium-binding protein, calcineurin
 CC -beta. A novel interferon receptor binding protein, IR1B1 (see AAW64199),
 CC of the invention shows marked homology, e.g. calcium binding sites (E-F
 CC handles), to calcineurin-beta; amino acid residues 50-171 show 59.8%
 CC similarity and 32.5% identity. IR1B1 polypeptides and polynucleotides can
 CC be used to develop products for modulating sensitivity to interferon,
 CC e.g. in cancer therapy and for prolonging graft survival
 XX
 SQ Sequence 170 AA;

Query Match 100.0%; Score 870; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 7.9e-83;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 61
 QY 61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 121
 QY 121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 122>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:04:17 ; Search time 39 Seconds
(without alignments)
416.939 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKMVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 870 | 100.0 | 170 | 1 | A33391 | calcineurin regula |
| 2 | 870 | 100.0 | 170 | 1 | S34127 | calcineurin regula |
| 3 | 870 | 100.0 | 216 | 1 | S42716 | calcineurin regula |
| 4 | 865 | 99.4 | 170 | 1 | JC1220 | calcineurin regula |
| 5 | 784 | 90.1 | 170 | 2 | JC7242 | calcineurin regula |
| 6 | 766 | 88.0 | 170 | 2 | JC5174 | calcineurin regula |
| 7 | 762 | 87.6 | 170 | 2 | A44307 | calcineurin regula |
| 8 | 704 | 80.9 | 369 | 2 | T22708 | hypothetical prote |
| 9 | 702 | 80.7 | 179 | 2 | JC1221 | calcineurin regula |
| 10 | 699 | 80.3 | 176 | 2 | JQ1232 | calcineurin regula |
| 11 | 620 | 71.3 | 165 | 2 | PS0261 | calcineurin regula |
| 12 | 528 | 60.7 | 174 | 2 | T47245 | calcineurin regula |
| 13 | 496 | 57.0 | 175 | 2 | JH0462 | phosphoprotein pho |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 14 | 483 | 55.5 | 174 | 2 | T41632 | probable calcineur |
| 15 | 316.5 | 36.4 | 213 | 2 | T31775 | hypothetical prote |
| 16 | 303.5 | 34.9 | 195 | 2 | T28047 | hypothetical prote |
| 17 | 255 | 29.3 | 311 | 2 | T21563 | hypothetical prote |
| 18 | 233.5 | 26.8 | 150 | 2 | T07122 | calmodulin CAM5 - |
| 19 | 233.5 | 26.8 | 151 | 2 | A71409 | calmodulin 8 [impo |
| 20 | 230 | 26.4 | 591 | 2 | S54788 | calcium-stimulated |
| 21 | 229.5 | 26.4 | 149 | 2 | S35187 | calmodulin 6 - Ara |
| 22 | 228.5 | 26.3 | 149 | 1 | S53006 | calmodulin - leaf |
| 23 | 228.5 | 26.3 | 149 | 1 | MCPZDC | calmodulin - carro |
| 24 | 228.5 | 26.3 | 149 | 1 | S22503 | calmodulin [simila |
| 25 | 228.5 | 26.3 | 149 | 1 | S22971 | calmodulin - trump |
| 26 | 228.5 | 26.3 | 149 | 1 | S40301 | calmodulin - red b |
| 27 | 228.5 | 26.3 | 149 | 1 | S70768 | calmodulin CAM81 - |
| 28 | 228.5 | 26.3 | 149 | 2 | T47417 | calmodulin 7 [simi |
| 29 | 228.5 | 26.3 | 149 | 2 | H84667 | calmodulin (cam2) |
| 30 | 227.5 | 26.1 | 149 | 1 | MCBH | calmodulin - barle |
| 31 | 227.5 | 26.1 | 149 | 1 | MCWT | calmodulin - wheat |
| 32 | 227.5 | 26.1 | 149 | 2 | S24952 | calmodulin 1 (clon |
| 33 | 226.5 | 26.0 | 149 | 2 | S58311 | calmodulin - Biden |
| 34 | 226.5 | 26.0 | 149 | 2 | S60237 | calmodulin PCM2/PC |
| 35 | 225.5 | 25.9 | 149 | 1 | MCZQF | calmodulin - malar |
| 36 | 224.5 | 25.8 | 149 | 1 | MCAA | calmodulin - alfal |
| 37 | 224.5 | 25.8 | 149 | 2 | S22860 | calmodulin 2 (clon |
| 38 | 223.5 | 25.7 | 149 | 1 | I51202 | calmodulin - duck |
| 39 | 223.5 | 25.7 | 149 | 1 | MCCH | calmodulin - chick |
| 40 | 223.5 | 25.7 | 149 | 1 | MCEE | calmodulin - elect |
| 41 | 223.5 | 25.7 | 149 | 1 | MCHU | calmodulin [valida |
| 42 | 223.5 | 25.7 | 149 | 1 | MCRT | calmodulin [valida |
| 43 | 223.5 | 25.7 | 149 | 2 | JC1305 | calmodulin - Japan |
| 44 | 223.5 | 25.7 | 149 | 2 | I51402 | calmodulin - Afric |
| 45 | 223.5 | 25.7 | 149 | 2 | S37707 | calmodulin - mouse |

ALIGNMENTS

RESULT 1

A33391

calcineurin regulatory chain - human

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Homo sapiens (man)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C;Accession: A33391

R;Guerini, D.; Krinks, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.

DNA 8, 675-682, 1989

A;Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding subunit of the Ca(2+)/calmodulin-stimulated protein phosphatase.

A;Reference number: A33391; MUID:90126237; PMID:2558868

A;Accession: A33391

A;Molecule type: mRNA

A;Residues: 1-170 <GUE>

A;Cross-references: UNIPROT:P06705; GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705

C;Genetics:

A;Gene: GDB:PPP3R1; CALNB

A;Cross-references: GDB:136804; OMIM:601302
A;Map position: 2p16-2p15
C;Complex: heterodimer with calcineurin catalytic chain
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Modified site: aspartic acid (Asn) #status predicted
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status predicted

Query Match 100.0%; Score 870; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 6e-56;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 60
      |||
Db      2 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDK EQKLRF AFRIYDMDKDGYISNGELFQVLKMMVG 120
      |||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDK EQKLRF AFRIYDMDKDGYISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDG DGRISFEEFC AVVGGLDIHKKMVVDV 169
      |||
Db    122 NNLKDTQLQQIVDKTIINADKDG DGRISFEEFC AVVGGLDIHKKMVVDV 170
```

RESULT 2

S34127

calcineurin regulatory chain [validated] - bovine

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: I45831; JT0297; S34127

R;Nargang, C.E.; Bottorff, D.A.; Adachi, K.

DNA Seq. 4, 313-318, 1994

A;Title: Isolation and characterization of a cDNA clone coding for the calcium-binding subunit of calcineurin from bovine brain: an identical amino acid sequence to the human protein.

A;Reference number: I45831; MUID:95102111; PMID:7803816

A;Accession: I45831

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

us-09-763-720-1.rup

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:07:47 ; Search time 175 Seconds
(without alignments)
494.522 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|------------|--------------------|
| 1 | 870 | 100.0 | 169 | 1 | CALB_BOVIN | P63099 bos taurus |
| 2 | 870 | 100.0 | 169 | 1 | CALB_HUMAN | P63098 homo sapien |
| 3 | 870 | 100.0 | 169 | 1 | CALB_RAT | P63100 rattus norv |
| 4 | 870 | 100.0 | 170 | 2 | Q66HZ0 | Q66hz0 brachydanio |
| 5 | 870 | 100.0 | 170 | 2 | Q6DJJ3 | Q6djj3 xenopus lae |
| 6 | 870 | 100.0 | 170 | 2 | Q6VN50 | Q6vn50 xenopus tro |
| 7 | 870 | 100.0 | 170 | 2 | Q6VN51 | Q6vn51 gallus gall |
| 8 | 865 | 99.4 | 169 | 1 | CALB_MOUSE | Q63810 mus musculu |
| 9 | 860 | 98.9 | 170 | 2 | Q7T063 | Q7t063 xenopus lae |
| 10 | 795 | 91.4 | 765 | 2 | Q86YQ0 | Q86yq0 homo sapien |
| 11 | 791 | 90.9 | 170 | 2 | Q9NkW7 | Q9nkw7 patinopecte |
| 12 | 769 | 88.4 | 169 | 2 | Q7PQ91 | Q7pq91 anopheles g |
| 13 | 766 | 88.0 | 170 | 1 | CALC_DROME | Q24214 drosophila |
| 14 | 762 | 87.6 | 170 | 1 | CALB_DROME | P48451 drosophila |
| 15 | 762 | 87.6 | 170 | 2 | Q95P81 | Q95p81 bombyx mori |
| 16 | 734.5 | 84.4 | 169 | 2 | Q86H16 | Q86h16 schistosoma |
| 17 | 733 | 84.3 | 169 | 1 | CALC_HUMAN | Q961z3 homo sapien |
| 18 | 732.5 | 84.2 | 169 | 2 | Q9NFN1 | Q9nfn1 schistosoma |
| 19 | 707 | 81.3 | 170 | 2 | Q7YRC9 | Q7yrc9 macaca mula |
| 20 | 704 | 80.9 | 171 | 2 | Q20804 | Q20804 caenorhabdi |
| 21 | 702 | 80.7 | 178 | 1 | CALC_MOUSE | Q63811 mus musculu |

| | | | | | us-09-763-720-1.rup | |
|----|-------|------|-----|---|---------------------|--------------------|
| 22 | 699 | 80.3 | 175 | 1 | CALC_RAT | P28470 rattus norv |
| 23 | 580 | 66.7 | 115 | 2 | Q99LQ9 | Q99LQ9 mus musculu |
| 24 | 544 | 62.5 | 173 | 1 | CALB_YARLI | Q6cge6 yarrowia li |
| 25 | 540.5 | 62.1 | 174 | 1 | CALB_NEUCR | P87072 neurospora |
| 26 | 528 | 60.7 | 175 | 1 | CALB_CRYNE | Q9hde1 cryptococcu |
| 27 | 517 | 59.4 | 177 | 1 | CALB_NAEGR | P42322 naegleria g |
| 28 | 499 | 57.4 | 175 | 1 | CALB_ASHGO | Q757b7 ashbya goss |
| 29 | 496 | 57.0 | 174 | 1 | CALB_YEAST | P25296 saccharomyc |
| 30 | 483 | 55.5 | 174 | 1 | CALB_SCHPO | Q9uu93 schizosacch |
| 31 | 483 | 55.5 | 175 | 1 | CALB_CANGA | Q6flu4 candida gla |
| 32 | 475 | 54.6 | 175 | 1 | CALB_KLULA | Q874t7 kluyveromyc |
| 33 | 469 | 53.9 | 174 | 1 | CALB_DEBHA | Q6bws8 debaryomyce |
| 34 | 451 | 51.8 | 177 | 2 | Q8MQT6 | Q8mq6 toxoplasma |
| 35 | 443.5 | 51.0 | 169 | 2 | Q867N3 | Q867n3 paramecium |
| 36 | 442.5 | 50.9 | 180 | 2 | Q9GP83 | Q9gp83 dictyosteli |
| 37 | 436 | 50.1 | 177 | 2 | Q86RA7 | Q86ra7 plasmodium |
| 38 | 436 | 50.1 | 179 | 2 | Q8IKV9 | Q8ikv9 plasmodium |
| 39 | 415.5 | 47.8 | 166 | 2 | Q7RP38 | Q7rp38 plasmodium |
| 40 | 372 | 42.8 | 175 | 2 | Q9U0X7 | Q9u0x7 leishmania |
| 41 | 340.5 | 39.1 | 194 | 1 | CHP1_MOUSE | P61022 mus musculu |
| 42 | 340.5 | 39.1 | 194 | 1 | CHP1_RAT | P61023 rattus norv |
| 43 | 338.5 | 38.9 | 193 | 2 | Q6DK70 | Q6dk70 xenopus tro |
| 44 | 338.5 | 38.9 | 193 | 2 | Q6DKL7 | Q6dk17 xenopus lae |
| 45 | 337.5 | 38.8 | 194 | 1 | CHP1_HUMAN | Q99653 homo sapien |

ALIGNMENTS

RESULT 1

CALB_BOVIN

ID CALB_BOVIN STANDARD; PRT; 169 AA.
AC P63099; P06705; P15117; Q08044;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE 1).
GN Name=PPP3R1; Synonyms=CNA2, CNB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95102111; PubMed=7803816;
RA Nargang C.E., Bottorff D.A., Adachi K.;
RT "Isolation and characterization of a cDNA clone coding for the
RT calcium-binding subunit of calcineurin from bovine brain: an identical
RT amino acid sequence to the human protein.";
RL DNA Seq. 4:313-318(1994).
RN [2]
RP SEQUENCE OF 1-168.
RC TISSUE=Brain;
RX MEDLINE=84132092; PubMed=6321184;
RA Aitken A., Klee C.B., Cohen P.;
RT "The structure of the B subunit of calcineurin.";
RL Eur. J. Biochem. 139:663-671(1984).
RN [3]
RP CALCIUM-BINDING DATA.

us-09-763-720-1.rup

RX MEDLINE=80101597; PubMed=293720;
RA Klee C.B., Crouch T.H., Krinks M.H.;
RT "Calcineurin: a calcium- and calmodulin-binding protein of the nervous
RT system.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH FKBP1A.
RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;
RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;
RT "X-ray structure of calcineurin inhibited by the immunophilin-
RT immunosuppressant FKBP12-FK506 complex.";
RL Cell 82:507-522(1995).
CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC calmodulin stimulated protein phosphatase. Confers calcium
CC sensitivity.
CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC subunit (B).
CC -!- MISCELLANEOUS: This protein has four functional calcium-binding
CC sites.
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X71666; CAA50659.1; -.
DR PIR; I45831; S34127.
DR PDB; 1TCO; X-ray; B=1-169.
DR GO; GO:0005955; C:calcineurin complex; NAS.
DR GO; GO:0005509; F:calcium ion binding; NAS.
DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; 4.
KW 3D-structure; Calcium-binding; Direct protein sequencing; Lipoprotein;
KW Myristate; Repeat.
FT INIT_MET 0 0
FT LIPID 1 1 N-myristoyl glycine.
FT CA_BIND 30 41 EF-hand 1.
FT CA_BIND 62 73 EF-hand 2.
FT CA_BIND 99 110 EF-hand 3.
FT CA_BIND 140 151 EF-hand 4.
FT CONFLICT 11 11 C -> M (in Ref. 2).
FT CONFLICT 153 153 C -> S (in Ref. 2).
FT HELIX 16 29
FT TURN 31 32
FT STRAND 36 37
FT HELIX 39 42
FT TURN 43 44
FT HELIX 46 49
FT TURN 50 50
FT TURN 52 53

us-09-763-720-1.rup

```
FT  HELIX      54      61
FT  TURN       63      64
FT  STRAND     69      70
FT  HELIX      71      78
FT  HELIX      79      81
FT  TURN       83      84
FT  HELIX      87      98
FT  TURN     100     101
FT  STRAND    105     106
FT  HELIX    108     119
FT  TURN    120     121
FT  HELIX    125     139
FT  TURN    141     142
FT  STRAND    147     148
FT  HELIX    149     156
FT  HELIX    157     159
FT  HELIX    161     164
SQ  SEQUENCE   169 AA;  19169 MW;  749141BD0434C90C CRC64;
```

Query Match 100.0%; Score 870; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.1e-52;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQQNPLVQRVIDI 60
      |||
DB      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQQNPLVQRVIDI 60

QY     61 FDTDGNGEVDFKEFIEGVVSQFSVKGDKLRFQAFRIYDMKDGYSISNGELFQVLKMMVG 120
      |||
DB     61 FDTDGNGEVDFKEFIEGVVSQFSVKGDKLRFQAFRIYDMKDGYSISNGELFQVLKMMVG 120

QY    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
      |||
DB    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
```

RESULT 2

CALB_HUMAN

```
ID  CALB_HUMAN      STANDARD;      PRT;   169 AA.
AC  P63098; P06705; P15117; Q08044;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE  subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE  1).
GN  Name=PPP3R1; Synonyms=CNA2, CNB;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90126237; PubMed=2558868;
RA  Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;
RT  "Isolation and sequence of a cDNA clone for human calcineurin B, the
RT  Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein
RT  phosphatase.";
RL  DNA 8:675-682(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT  "Cloning of human full open reading frames in Gateway(TM) system entry
```

RT vector (pDONR201).";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
 RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,
 RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
 RA Bacquet R., Villafranca J.E.;
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-
 RT calcineurin complex.";
 RL Nature 378:641-644(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) IN COMPLEX WITH PPIA.
 RX PubMed=12218175; DOI=10.1073/pnas.192206699;
 RA Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.;
 RT "Crystal structure of calcineurin-cyclophilin-cyclosporin shows common
 RT but distinct recognition of immunophilin-drug complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042(2002).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) IN COMPLEX WITH PPIA.
 RX PubMed=12357034; DOI=10.1073/pnas.212504399;
 RA Jin L., Harrison S.C.;
 RT "Crystal structure of human calcineurin complexed with cyclosporin A
 RT and human cyclophilin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526(2002).
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
 CC calmodulin stimulated protein phosphatase. Confers calcium
 CC sensitivity.
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
 CC subunit (B).
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding
 CC sites.
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; M30773; AAB08721.1; -.
 DR EMBL; BC027913; AAH27913.1; -.
 DR EMBL; CR456938; CAG33219.1; -.
 DR PIR; A33391; A33391.
 DR PDB; 1AUI; X-ray; B=1-169.
 DR PDB; 1M63; X-ray; B/F=1-169.
 DR PDB; 1MF8; X-ray; B=1-169.
 DR OGP; P63098; -.
 DR Genew; HGNC:9317; PPP3R1.
 DR MIM; 601302; -.
 DR GO; GO:0005955; C:calcineurin complex; NAS.
 DR GO; GO:0005509; F:calcium ion binding; NAS.
 DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
 DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW 3D-structure; Calcium-binding; Lipoprotein; Myristate; Repeat.
 FT INIT_MET 0 0 By similarity.
 FT LIPID 1 1 N-myristoyl glycine (By similarity).
 FT CA_BIND 30 41 EF-hand 1.
 FT CA_BIND 62 73 EF-hand 2.
 FT CA_BIND 99 110 EF-hand 3.
 FT CA_BIND 140 151 EF-hand 4.
 FT HELIX 16 29
 FT TURN 31 32
 FT STRAND 36 37
 FT HELIX 39 42
 FT TURN 43 44
 FT HELIX 46 49
 FT TURN 50 50
 FT TURN 52 53
 FT HELIX 54 61
 FT TURN 63 64
 FT STRAND 69 70
 FT HELIX 71 78
 FT HELIX 79 81
 FT TURN 83 84
 FT HELIX 87 98
 FT TURN 100 101
 FT STRAND 105 106
 FT HELIX 108 119
 FT TURN 120 121
 FT HELIX 125 139
 FT TURN 141 142
 FT STRAND 147 148
 FT HELIX 149 156
 FT HELIX 157 159
 FT HELIX 161 164
 SQ SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 100.0%; Score 870; DB 1; Length 169;
 Best Local similarity 100.0%; Pred. No. 8.1e-52;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GNEASYPLEMCSHFDADAIEKRLGKRFFKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GNEASYPLEMCSHFDADAIEKRLGKRFFKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60

QY     61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKEQKLRFQAFRIYDMKDGYSNGELFQVLKMMVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKEQKLRFQAFRIYDMKDGYSNGELFQVLKMMVG 120

QY    121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169

```

RESULT 3

CALB_RAT

```

ID  CALB_RAT      STANDARD;      PRT;      169 AA.
AC  P63100; P06705; P15117; Q08044;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE  subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE  1).
GN  Name=Ppp3r1; Synonyms=Cna2, Cnb;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RC  STRAIN=Fischer;
RA  Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RT  "Regulation of calcineurin phosphatase activity by the B subunit and
RT  carboxy-terminal inhibitory domains of the A subunit.";
RL  Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC  TISSUE=Brain, and Testis;
RX  MEDLINE=94153993; PubMed=8110831; DOI=10.1016/0167-4781(94)90031-0;
RA  Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT  "cDNA cloning of an alternatively spliced isoform of the regulatory
RT  subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
RT  B alpha 2).";
RL  Biochim. Biophys. Acta 1217:174-180(1994).
CC  -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC  calmodulin stimulated protein phosphatase. Confers calcium
CC  sensitivity.
CC  -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC  subunit (B).
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1;
CC  IsoId=P63100-1, P06705-1;
CC  Sequence=Displayed;
CC  Name=2;
CC  IsoId=P63100-2, P06705-2;
CC  Sequence=VSP_000729;
CC  -!- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC  -!- MISCELLANEOUS: This protein has four functional calcium-binding
CC  sites.
CC  -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC  -----

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

Query Match 100.0%; Score 870; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 8.1e-52;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQQNPLVQRVIDI | 60 |
| | | | |
| Db | 1 | GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPQLQQNPLVQRVIDI | 60 |
| Qy | 61 | FDTDGNGEVDKFKEFIEGVSQFSVKGDKEQKLRFARIYDMKDGYISNGELFQVLKMMVG | 120 |
| | | | |
| Db | 61 | FDTDGNGEVDKFKEFIEGVSQFSVKGDKEQKLRFARIYDMKDGYISNGELFQVLKMMVG | 120 |
| Qy | 121 | NNLKDTQLQQIVDKTIINADKDGGRISFEFCVVGGDIHKKMVVDV | 169 |
| | | | |
| Db | 121 | NNLKDTQLQQIVDKTIINADKDGGRISFEFCVVGGDIHKKMVVDV | 169 |

Page 8

us-09-763-720-1.rup

OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC081617; AAH81617.1; -.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 60
      |||
db      2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFARIYDMDKDGYISNGELFQVLKMMVG 120
      |||
db     62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFARIYDMDKDGYISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKMVDV 169
      |||

```

Db 122 NNLKDTQLQQIVDKTIINADKGDGRISFEEFCAVVGGLDIHKKMVVDV 170

RESULT 5

Q6DJJ3

ID Q6DJJ3 PRELIMINARY; PRT; 170 AA.

AC Q6DJJ3;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MGC82148 protein.

GN Name=MGC82148;

OS *Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;

OC Xenopodinae; *Xenopus*.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*

RT initiative.";

RL Dev. Dyn. 225:384-391(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075185; AAH75185.1; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR InterPro; IPR001751; CaBP_S100.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF_Hand_like.

DR InterPro; IPR008080; Parvalbumin.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; efhand; 4.

```

DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium; Calcium-binding.
SQ SEQUENCE 170 AA: 19300 MW: C904715DC0386056 CRC64:

```

Query Match 100.0%; Score 870; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.1e-52;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | | | | | | | | |
|----|-----|-----------------|-----------|-----------|----------|-------|------|-------|------|---------|---------------|-----|
| Qy | 1 | GNEASYPLEMCSHFD | AEIKRLGKR | FKKLDLDNS | GSLSVEEF | FMSLP | PELQ | QNPLV | QVR | VIDI | 60 | |
| | | | | | | | | | | | | |
| Db | 2 | GNEASYPLEMCSHFD | AEIKRLGKR | FKKLDLDNS | GSLSVEEF | FMSLP | PELQ | QNPLV | QVR | VIDI | 61 | |
| Qy | 61 | FDTDNGGEVDFKE | FI | EGVSQFS | VKGDKE | QKL | RFA | FRI | YDM | DKDGYIS | NGELFQVLKMMVG | 120 |
| | | | | | | | | | | | | |
| Db | 62 | FDTDNGGEVDFKE | FI | EGVSQFS | VKGDKE | QKL | RFA | FRI | YDM | DKDGYIS | NGELFQVLKMMVG | 121 |
| Qy | 121 | NNLKDTQLQQIV | DKTI | INADK | GDGRIS | FEEF | CAV | VGG | LDIH | KKM | VVDV | 169 |
| | | | | | | | | | | | | |
| Db | 122 | NNLKDTQLQQIV | DKTI | INADK | GDGRIS | FEEF | CAV | VGG | LDIH | KKM | VVDV | 170 |

Q6VN50

```

Q6VN50
ID Q6VN50; PRELIMINARY; PRT; 170 AA.
AC Q6VN50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1
DE (Hypothetical protein MGC75600).
GN Name=MGC75600;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Li W., Yu L., Zhao S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

```

us-09-763-720-1.rup

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY336972; AAQ16148.1; -.
DR EMBL; BC064854; AAH64854.1; -.
DR HSSP; P02618; 1B8R.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium; Calcium-binding; Hypothetical protein.
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.1e-52;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | GNEASYPLEMCSHFDAD E IKRLGKRFKKLDLDNSGSLSV E EFMSLPELQQNPLVQRVIDI | 60 |
| Db | 2 | GNEASYPLEMCSHFDAD E IKRLGKRFKKLDLDNSGSLSV E EFMSLPELQQNPLVQRVIDI | 61 |
| Qy | 61 | FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRF A FRIYDM D KDGYISNGELFQVLKMMVG | 120 |
| Db | 62 | FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRF A FRIYDM D KDGYISNGELFQVLKMMVG | 121 |
| Qy | 121 | NNLKDTQLQQIVDKTIINADKDG D GRISFEEFC A VVGGLDIHKKMVVDV | 169 |
| Db | 122 | NNLKDTQLQQIVDKTIINADKDG D GRISFEEFC A VVGGLDIHKKMVVDV | 170 |

RESULT 7
Q6VN51

```

Q6VN51      PRELIMINARY;      PRT;   170 AA.
AC   Q6VN51;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Protein phosphatase 3 regulatory subunit B alpha isoform type 1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bursa;

```

us-09-763-720-1.rup

RA Zhou G., Li W., Yu L., Zhao S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336970; AAQ16146.1; -.
 DR HSSP; P02618; 1B8R.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR InterPro; IPR008080; Parvalbumin.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 4.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium; Calcium-binding.
 SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI | 60 |
| | | | |
| Db | 2 | GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI | 61 |
| Qy | 61 | FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYSNGELFQVLKMMVG | 120 |
| | | | |
| Db | 62 | FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYSNGELFQVLKMMVG | 121 |
| Qy | 121 | NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV | 169 |
| | | | |
| Db | 122 | NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV | 170 |

us-09-763-720-1.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 51 Seconds
(without alignments)
1102.778 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|-----------------|-------------------|
| 1 | 870 | 100.0 | 170 | 13 | US-10-109-885-3 | Sequence 3, Appli |
| 2 | 870 | 100.0 | 170 | 14 | US-10-309-280-3 | Sequence 3, Appli |
| 3 | 733 | 84.3 | 170 | 15 | US-10-239-572-2 | Sequence 2, Appli |

| us-09-763-720-1.rapb | | | | | |
|----------------------|-------|------|-----|-------------------------|-------------------|
| 4 | 733 | 84.3 | 173 | 15 US-10-094-749-3200 | Sequence 3200, Ap |
| 5 | 733 | 84.3 | 187 | 11 US-09-764-875-845 | Sequence 845, App |
| 6 | 733 | 84.3 | 189 | 9 US-09-764-881-148 | Sequence 148, App |
| 7 | 733 | 84.3 | 189 | 10 US-09-764-891-3897 | Sequence 3897, Ap |
| 8 | 733 | 84.3 | 189 | 10 US-09-764-881-148 | Sequence 148, App |
| 9 | 733 | 84.3 | 189 | 11 US-09-764-875-1133 | Sequence 1133, Ap |
| 10 | 733 | 84.3 | 189 | 15 US-10-242-747-148 | Sequence 148, App |
| 11 | 733 | 84.3 | 189 | 15 US-10-158-057-242 | Sequence 242, App |
| 12 | 733 | 84.3 | 189 | 15 US-10-158-057-317 | Sequence 317, App |
| 13 | 501 | 57.6 | 197 | 15 US-10-369-493-13106 | Sequence 13106, A |
| 14 | 496 | 57.0 | 175 | 15 US-10-369-493-22220 | Sequence 22220, A |
| 15 | 429.5 | 49.4 | 195 | 15 US-10-369-493-22782 | Sequence 22782, A |
| 16 | 429 | 49.3 | 185 | 15 US-10-369-493-4075 | Sequence 4075, Ap |
| 17 | 373.5 | 42.9 | 178 | 14 US-10-342-224-54 | Sequence 54, Appl |
| 18 | 340.5 | 39.1 | 195 | 9 US-09-999-602-3 | Sequence 3, Appli |
| 19 | 340.5 | 39.1 | 195 | 17 US-10-482-838-18 | Sequence 18, Appl |
| 20 | 337.5 | 38.8 | 194 | 17 US-10-480-847-6 | Sequence 6, Appli |
| 21 | 337.5 | 38.8 | 195 | 9 US-09-999-602-4 | Sequence 4, Appli |
| 22 | 337.5 | 38.8 | 195 | 17 US-10-482-838-17 | Sequence 17, Appl |
| 23 | 316.5 | 36.4 | 213 | 15 US-10-369-493-6287 | Sequence 6287, Ap |
| 24 | 303.5 | 34.9 | 195 | 15 US-10-369-493-6454 | Sequence 6454, Ap |
| 25 | 292 | 33.6 | 207 | 9 US-09-764-881-145 | Sequence 145, App |
| 26 | 292 | 33.6 | 207 | 10 US-09-764-881-145 | Sequence 145, App |
| 27 | 292 | 33.6 | 207 | 11 US-09-764-875-1138 | Sequence 1138, Ap |
| 28 | 292 | 33.6 | 207 | 15 US-10-242-747-145 | Sequence 145, App |
| 29 | 292 | 33.6 | 207 | 15 US-10-158-057-320 | Sequence 320, App |
| 30 | 291 | 33.4 | 196 | 17 US-10-482-838-9 | Sequence 9, Appli |
| 31 | 291 | 33.4 | 210 | 11 US-09-764-875-854 | Sequence 854, App |
| 32 | 289 | 33.2 | 199 | 15 US-10-276-774-2317 | Sequence 2317, Ap |
| 33 | 284 | 32.6 | 194 | 16 US-10-322-281-506 | Sequence 506, App |
| 34 | 280 | 32.2 | 196 | 17 US-10-482-838-16 | Sequence 16, Appl |
| 35 | 248 | 28.5 | 175 | 15 US-10-424-599-185489 | Sequence 185489, |
| 36 | 240 | 27.6 | 208 | 15 US-10-425-114-57256 | Sequence 57256, A |
| 37 | 233 | 26.8 | 194 | 15 US-10-425-114-65892 | Sequence 65892, A |
| 38 | 231.5 | 26.6 | 218 | 15 US-10-425-114-47771 | Sequence 47771, A |
| 39 | 230.5 | 26.5 | 171 | 16 US-10-437-963-185345 | Sequence 185345, |
| 40 | 230.5 | 26.5 | 174 | 15 US-10-425-114-59559 | Sequence 59559, A |
| 41 | 230.5 | 26.5 | 181 | 15 US-10-425-114-46972 | Sequence 46972, A |
| 42 | 230.5 | 26.5 | 183 | 15 US-10-425-114-44959 | Sequence 44959, A |
| 43 | 230.5 | 26.5 | 183 | 15 US-10-425-114-56162 | Sequence 56162, A |
| 44 | 230.5 | 26.5 | 183 | 15 US-10-425-114-60654 | Sequence 60654, A |
| 45 | 230.5 | 26.5 | 184 | 15 US-10-425-114-56165 | Sequence 56165, A |

ALIGNMENTS

RESULT 1

US-10-109-885-3

; Sequence 3, Application US/10109885

; Publication No. US20020119129A1

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: CHEBATH, Judith

; APPLICANT: ABRAMOVITCH, Carolina

; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND

METHODS OF

; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON

; FILE REFERENCE: REVEL=14A

; CURRENT APPLICATION NUMBER: US/10/109,885

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: US/09/341,640

; PRIOR FILING DATE: 1999-10-18

```

;                               us-09-763-720-1.rapb
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-109-885-3

```

```

Query Match          100.0%; Score 870; DB 13; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLPELQQNPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKKEQKLRFARIYDMKDGYSINGELFQVLKMMVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKKEQKLRFARIYDMKDGYSINGELFQVLKMMVG 121

Qy    121>NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGLDIHKKMVVDV 169
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122>NNLKDTQLQQIVDKTIINADKGDGRISFEEFCVVGGLDIHKKMVVDV 170

```

```

RESULT 2
US-10-309-280-3
; Sequence 3, Application US/10309280
; Publication No. US20030176678A1
; GENERAL INFORMATION:
;   APPLICANT: REVEL, Michel
;   APPLICANT: CHEBATH, Judith
;   APPLICANT: ABRAMOVITCH, Carolina
;   TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
METHODS OF
;   TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
;   FILE REFERENCE: REVEL=14A
;   CURRENT APPLICATION NUMBER: US/10/309,280
;   CURRENT FILING DATE: 2002-12-04
;   PRIOR APPLICATION NUMBER: US/09/341,640
;   PRIOR FILING DATE: 1999-10-18
;   PRIOR APPLICATION NUMBER: PCT/US98/00671
;   PRIOR FILING DATE: 1998-01-15
;   PRIOR APPLICATION NUMBER: US 60/035,636
;   PRIOR FILING DATE: 1997-01-15
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-309-280-3

```

```

Query Match          100.0%; Score 870; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;

```


us-09-763-720-1.rapb

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQNPLVQRVIDI 60
        |||
Db      2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQNPLVQRVIDI 61
        |||
Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDKLRFQAFRIYDMDKDGYSNGELFQVLKMMVG 120
        |||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDKLRFQAFRIYDMDKDGYSNGELFQVLKMMVG 121
        |||
Qy    121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
        |||
Db    122>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170
```

A;Residues: 1-170 <NA2>
A;Cross-references: UNIPROT:P06705; EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969
R;Aitken, A.; Klee, C.B.; Cohen, P.
Eur. J. Biochem. 139, 663-671, 1984
A;Title: The structure of the B-subunit of calcineurin.
A;Reference number: JT0297; MUID:84132092; PMID:6321184
A;Accession: JT0297
A;Molecule type: protein
A;Residues: 2-11,'M',13-153,'S',155-169 <AIT>
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A66708; PDB:1TCO
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.
Cell 82, 507-522, 1995
A;Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex.
A;Reference number: A56967; MUID:95360994; PMID:7543369
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation
F;2-170/Product: calcineurin regulatory chain #status experimental <MAT>
F;18-49/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>
F;87-119/Domain: calmodulin repeat homology <EF3>
F;128-160/Domain: calmodulin repeat homology <EF4>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental
F;3/Modified site: aspartic acid (Asn) #status predicted
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experimental
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experimental
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status experimental
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status experimental

Query Match 100.0%; Score 870; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 6e-56;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60
      |||||||
Db      2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 120
      |||||||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
      |||||||

```


Db 108 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 167

Qy 121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169
 |||

Db 168 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 216

RESULT 4

JC1220

calcineurin regulatory chain, brain - mouse

N;Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1;

phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JC1220

R;Ueki, K.; Muramatsu, T.; Kincaid, R.L.

Biochem. Biophys. Res. Commun. 187, 537-543, 1992

A;Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).

A;Reference number: JC1220; MUID:92392379; PMID:1325794

A;Accession: JC1220

A;Molecule type: mRNA

A;Residues: 1-170 <UEK>

A;Cross-references: UNIPROT:Q63810; GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

A;Experimental source: brain

C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneural calcium-regulated signaling.

C;Genetics:

A;Gene: PP2B-beta-1

C;Complex: heterodimer with calcineurin catalytic chain

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation

F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>

F;18-49/Domain: calmodulin repeat homology <EF1>

F;50-82/Domain: calmodulin repeat homology <EF2>

F;87-119/Domain: calmodulin repeat homology <EF3>

F;128-160/Domain: calmodulin repeat homology <EF4>

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 99.4%; Score 865; DB 1; Length 170;

Best Local Similarity 99.4%; Pred. No. 1.4e-55;

Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60
 |:|

Db 2 GSEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 61

Qy 61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 120
 |||

Db 62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 121

Qy 121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169
 |||

Db 122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 170

us-09-763-720-1.ra1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 22 Seconds
(without alignments)
573.441 Million cell updates/sec

Title: US-09-763-720-1
Perfect score: 870
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|----------------------|-------------------|
| 1 | 870 | 100.0 | 169 | 3 | US-08-720-625-4 | Sequence 4, Appli |
| 2 | 870 | 100.0 | 170 | 3 | US-08-764-563-5 | Sequence 5, Appli |
| 3 | 702 | 80.7 | 179 | 3 | US-08-764-563-4 | Sequence 4, Appli |
| 4 | 517 | 59.4 | 177 | 3 | US-08-764-563-3 | Sequence 3, Appli |
| 5 | 496 | 57.0 | 174 | 1 | US-08-328-322-17 | Sequence 17, Appl |
| 6 | 488 | 56.1 | 157 | 1 | US-08-328-322-15 | Sequence 15, Appl |
| 7 | 469 | 53.9 | 204 | 4 | US-09-248-796A-18332 | Sequence 18332, A |
| 8 | 393 | 45.2 | 90 | 4 | US-09-513-999C-7071 | Sequence 7071, Ap |
| 9 | 321.5 | 37.0 | 233 | 4 | US-09-270-767-42765 | Sequence 42765, A |
| 10 | 284 | 32.6 | 196 | 3 | US-09-048-889-1 | Sequence 1, Appli |
| 11 | 242.5 | 27.9 | 145 | 3 | US-08-720-625-5 | Sequence 5, Appli |
| 12 | 233.5 | 26.8 | 150 | 3 | US-09-239-909-4 | Sequence 4, Appli |
| 13 | 225.5 | 25.9 | 149 | 3 | US-08-963-409-3 | Sequence 3, Appli |
| 14 | 223.5 | 25.7 | 149 | 3 | US-08-963-409-4 | Sequence 4, Appli |
| 15 | 223.5 | 25.7 | 149 | 3 | US-08-641-873-20 | Sequence 20, Appl |
| 16 | 223.5 | 25.7 | 149 | 4 | US-09-513-999C-7913 | Sequence 7913, Ap |
| 17 | 223.5 | 25.7 | 149 | 4 | US-09-949-016-6770 | Sequence 6770, Ap |

| | | | | us-09-763-720-1.ra | | |
|----|-------|------|-----|--------------------|---------------------|-------------------|
| 18 | 223.5 | 25.7 | 184 | 4 | US-09-949-016-7507 | Sequence 7507, Ap |
| 19 | 222.5 | 25.6 | 416 | 4 | US-09-989-025A-8 | Sequence 8, Appli |
| 20 | 221.5 | 25.5 | 150 | 3 | US-09-239-909-2 | Sequence 2, Appli |
| 21 | 220.5 | 25.3 | 148 | 4 | US-09-989-025A-4 | Sequence 4, Appli |
| 22 | 220.5 | 25.3 | 187 | 4 | US-09-949-016-6721 | Sequence 6721, Ap |
| 23 | 215.5 | 24.8 | 142 | 1 | US-07-951-715A-24 | Sequence 24, Appl |
| 24 | 215.5 | 24.8 | 142 | 2 | US-08-459-448A-24 | Sequence 24, Appl |
| 25 | 215.5 | 24.8 | 142 | 3 | US-08-459-595A-24 | Sequence 24, Appl |
| 26 | 215.5 | 24.8 | 142 | 3 | US-08-459-504B-24 | Sequence 24, Appl |
| 27 | 215.5 | 24.8 | 142 | 3 | US-08-459-444-24 | Sequence 24, Appl |
| 28 | 215.5 | 24.8 | 142 | 3 | US-09-547-422-24 | Sequence 24, Appl |
| 29 | 215.5 | 24.8 | 142 | 4 | US-09-988-462-24 | Sequence 24, Appl |
| 30 | 215 | 24.7 | 642 | 2 | US-08-818-253-2 | Sequence 2, Appli |
| 31 | 215 | 24.7 | 642 | 3 | US-08-818-252-2 | Sequence 2, Appli |
| 32 | 215 | 24.7 | 652 | 2 | US-08-818-253-4 | Sequence 4, Appli |
| 33 | 215 | 24.7 | 652 | 3 | US-08-818-252-4 | Sequence 4, Appli |
| 34 | 212 | 24.4 | 152 | 3 | US-08-963-409-5 | Sequence 5, Appli |
| 35 | 212 | 24.4 | 152 | 4 | US-09-949-016-6600 | Sequence 6600, Ap |
| 36 | 212 | 24.4 | 642 | 2 | US-08-818-253-6 | Sequence 6, Appli |
| 37 | 212 | 24.4 | 642 | 3 | US-08-818-252-6 | Sequence 6, Appli |
| 38 | 212 | 24.4 | 656 | 2 | US-08-818-253-8 | Sequence 8, Appli |
| 39 | 212 | 24.4 | 656 | 3 | US-08-818-252-8 | Sequence 8, Appli |
| 40 | 206.5 | 23.7 | 149 | 1 | US-08-100-874-2 | Sequence 2, Appli |
| 41 | 205 | 23.6 | 100 | 4 | US-09-270-767-46741 | Sequence 46741, A |
| 42 | 205 | 23.6 | 163 | 2 | US-08-698-805-8 | Sequence 8, Appli |
| 43 | 204.5 | 23.5 | 408 | 1 | US-07-951-715A-21 | Sequence 21, Appl |
| 44 | 204.5 | 23.5 | 408 | 2 | US-08-459-448A-21 | Sequence 21, Appl |
| 45 | 204.5 | 23.5 | 408 | 3 | US-08-459-595A-21 | Sequence 21, Appl |

ALIGNMENTS

RESULT 1

US-08-720-625-4

; Sequence 4, Application US/08720625

; Patent No. 6242587

GENERAL INFORMATION:

; APPLICANT: Naik, Ulhas P.

; APPLICANT: Parise, Leslie V.

; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN

; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bell, Seltzer, Park & Gibson

; STREET: P.O. Drawer 34009

; CITY: Charlotte

; STATE: No. 6242587th Carolina

; COUNTRY: USA

; ZIP: 28234

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,625

; FILING DATE:

; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

; NAME: Sibley, Kenneth D.

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5470-138

TELECOMMUNICATION INFORMATION:

```

;                                     us-09-763-720-1.rai
;   TELEPHONE: 919-420-2200
;   TELEFAX: 919-881-3175
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 169 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-720-625-4

```

```

Query Match          100.0%; Score 870; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 5.1e-81;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQQNPLVQRVIDI 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQQNPLVQRVIDI 60

QY      61 FDTDGNGEVDVFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYISNGELFQVLKMMVG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      61 FDTDGNGEVDVFKEFIEGVSVQSVKGDKEQKLRFARIYDMDKDGYISNGELFQVLKMMVG 120

QY      121 NNLKDTQLQQIVDKTIINADKDGGRISFEFCVAVGGGLDIHKKMVVDV 169
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB      121 NNLKDTQLQQIVDKTIINADKDGGRISFEFCVAVGGGLDIHKKMVVDV 169

```

RESULT 2

```

US-08-764-563-5
; Sequence 5, Application US/08764563
; Patent No. 6093565
; GENERAL INFORMATION:
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Goli, Surya K.
;   TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/764,563
;     FILING DATE: Herewith
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0178 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166

```

us-09-763-720-1.ra1

; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 461682
; US-08-764-563-5

Query Match 100.0%; Score 870; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.1e-81;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLP | 60 |
| | | | |
| Db | 2 | GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLP | 61 |
| Qy | 61 | FDTDGNGEVDFKEFIEGVSVQFSVKGDKLRFQFRIYDMDKDGYSNGELFQVLKMMVG | 120 |
| | | | |
| Db | 62 | FDTDGNGEVDFKEFIEGVSVQFSVKGDKLRFQFRIYDMDKDGYSNGELFQVLKMMVG | 121 |
| Qy | 121 | NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV | 169 |
| | | | |
| Db | 122 | NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV | 170 |